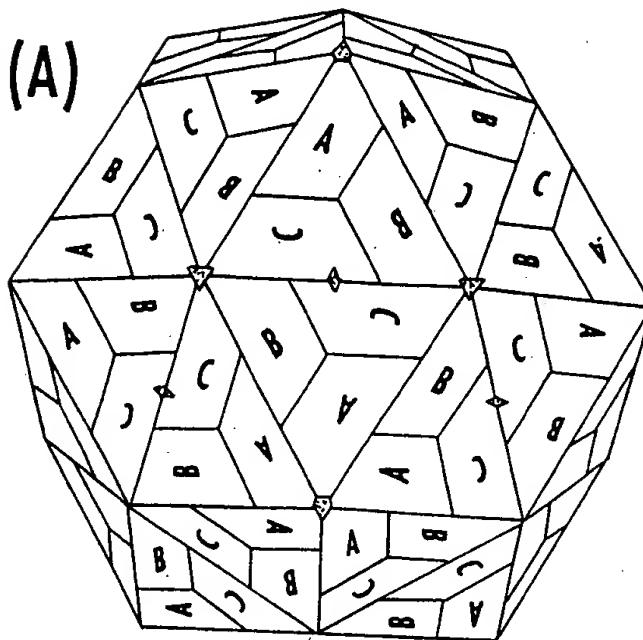




$T = 3$

Figure 1(A)



PICORNAVIRUS

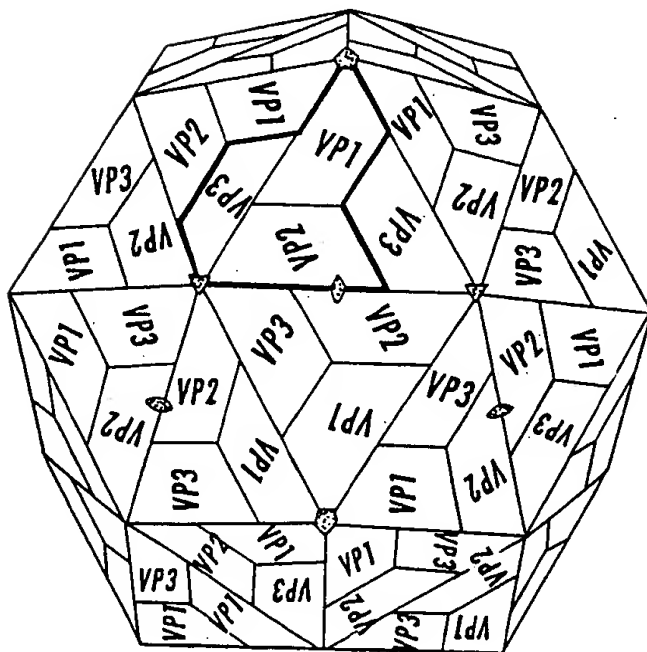


Figure 1(B)

COMOVIRUS

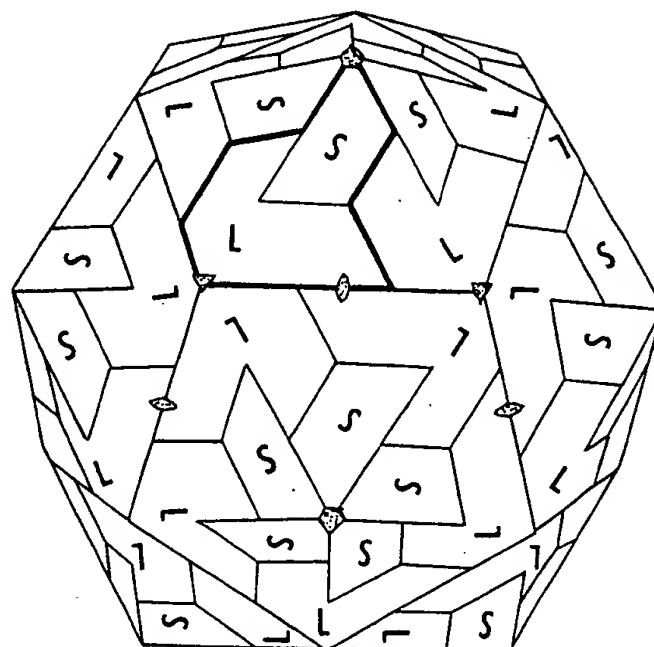


Figure 1(C)

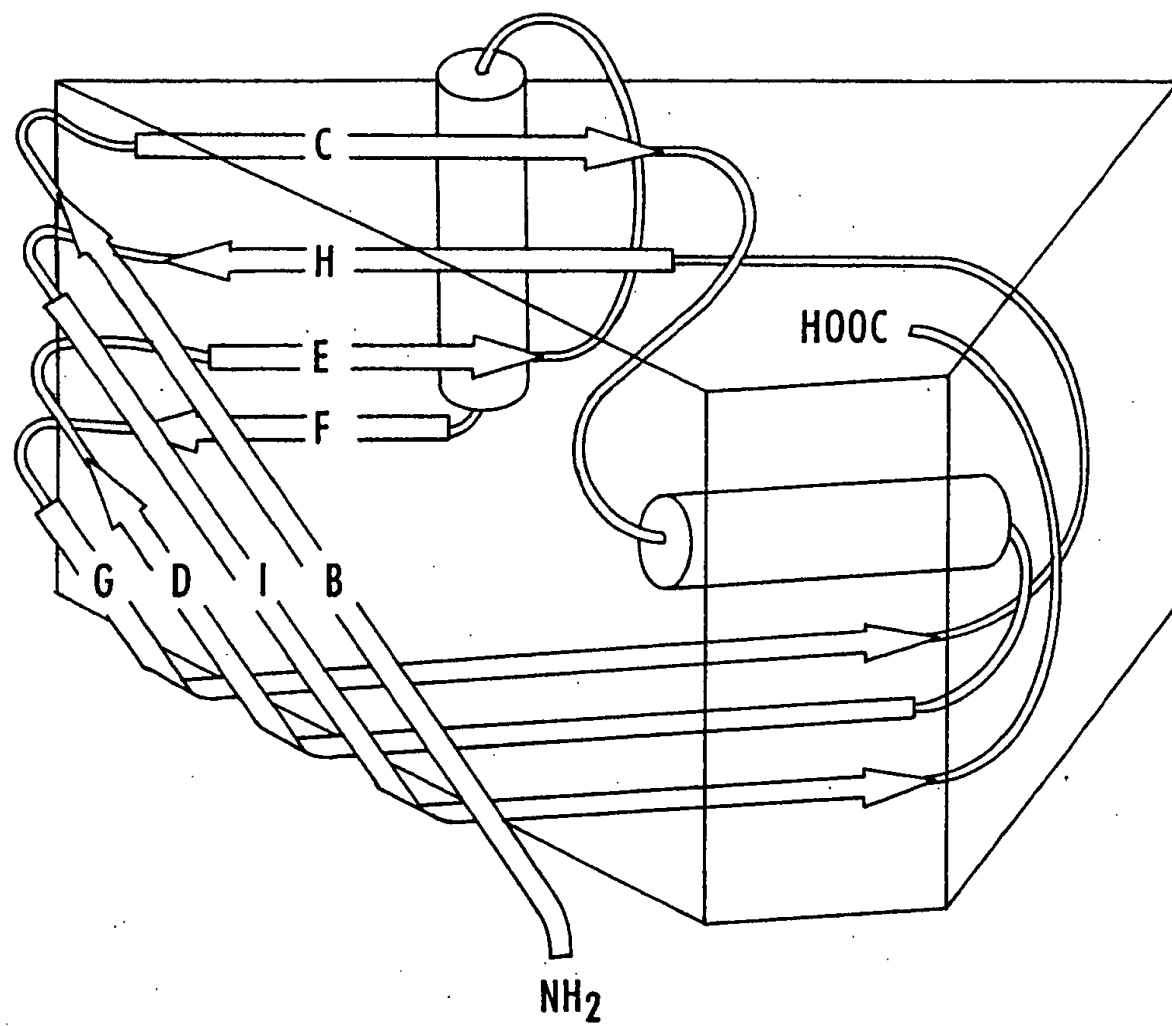


Figure 2

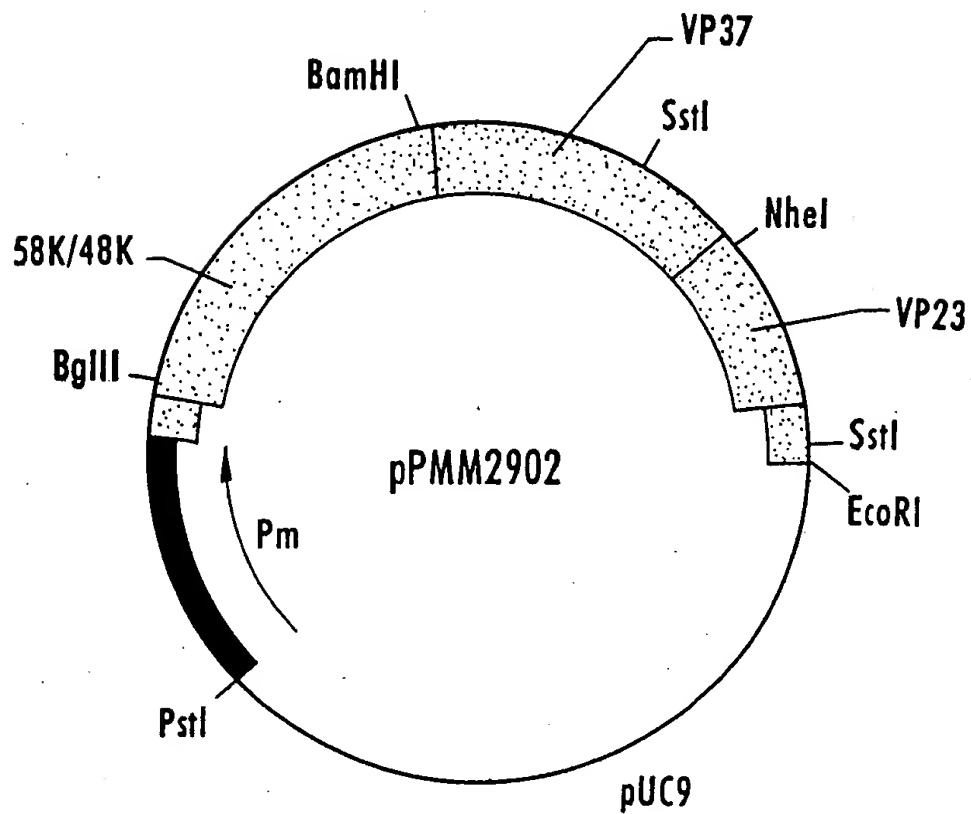


Figure 3(A)

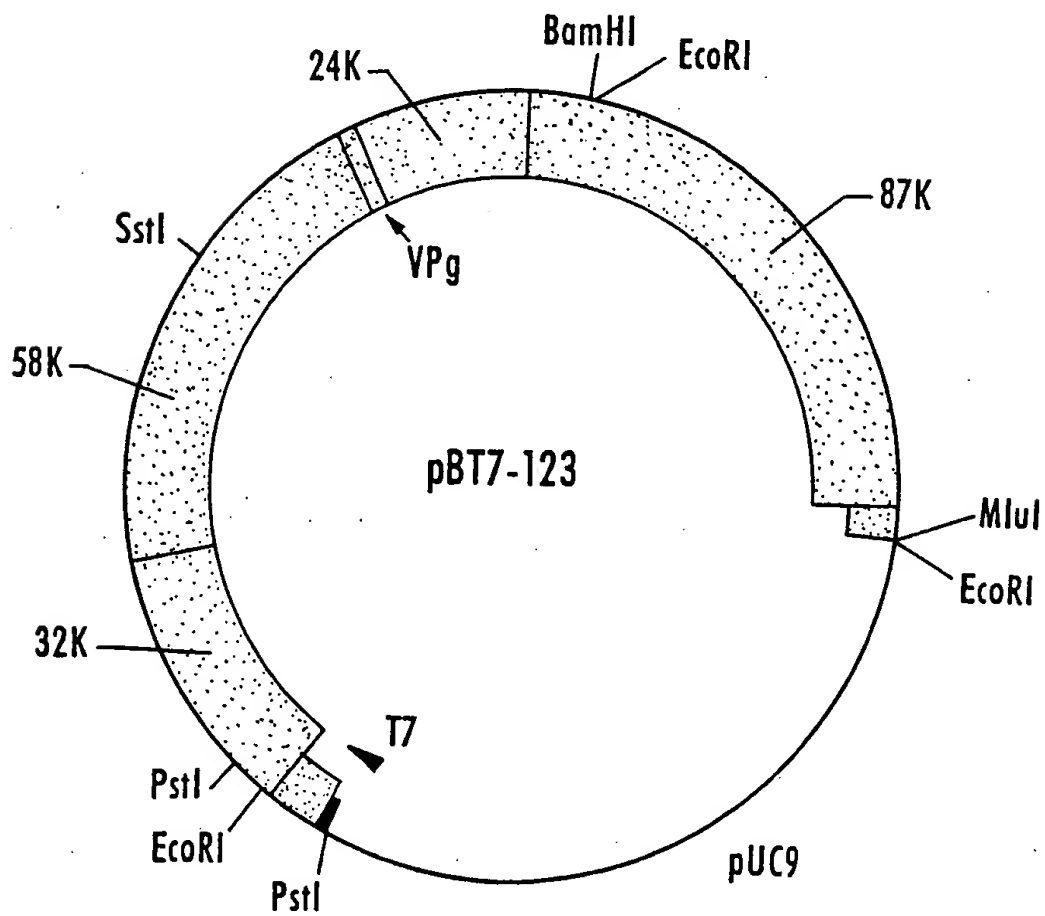


Figure 3(B)

1 5 10 15 20 25  
G P V C A E A S D V Y S P C M I A S T P P A P F S  
GGACCTGTTTGTGCTGAAGCCTCAGATGTGTATAGCCCATGTATGATAGCTAGCACTCCTCCTGCTCCATTTC  
2670 2700 NheI 2730

<----- β C ----->  
30 35 40  
D V T A V T F D L I N G K I T (SEQ ID NO: 6)  
GACGTTACAGCAGTAACCTTTTGACTTAATCAACGGCAAAATAACT (SEQ ID NO: 5)  
2760

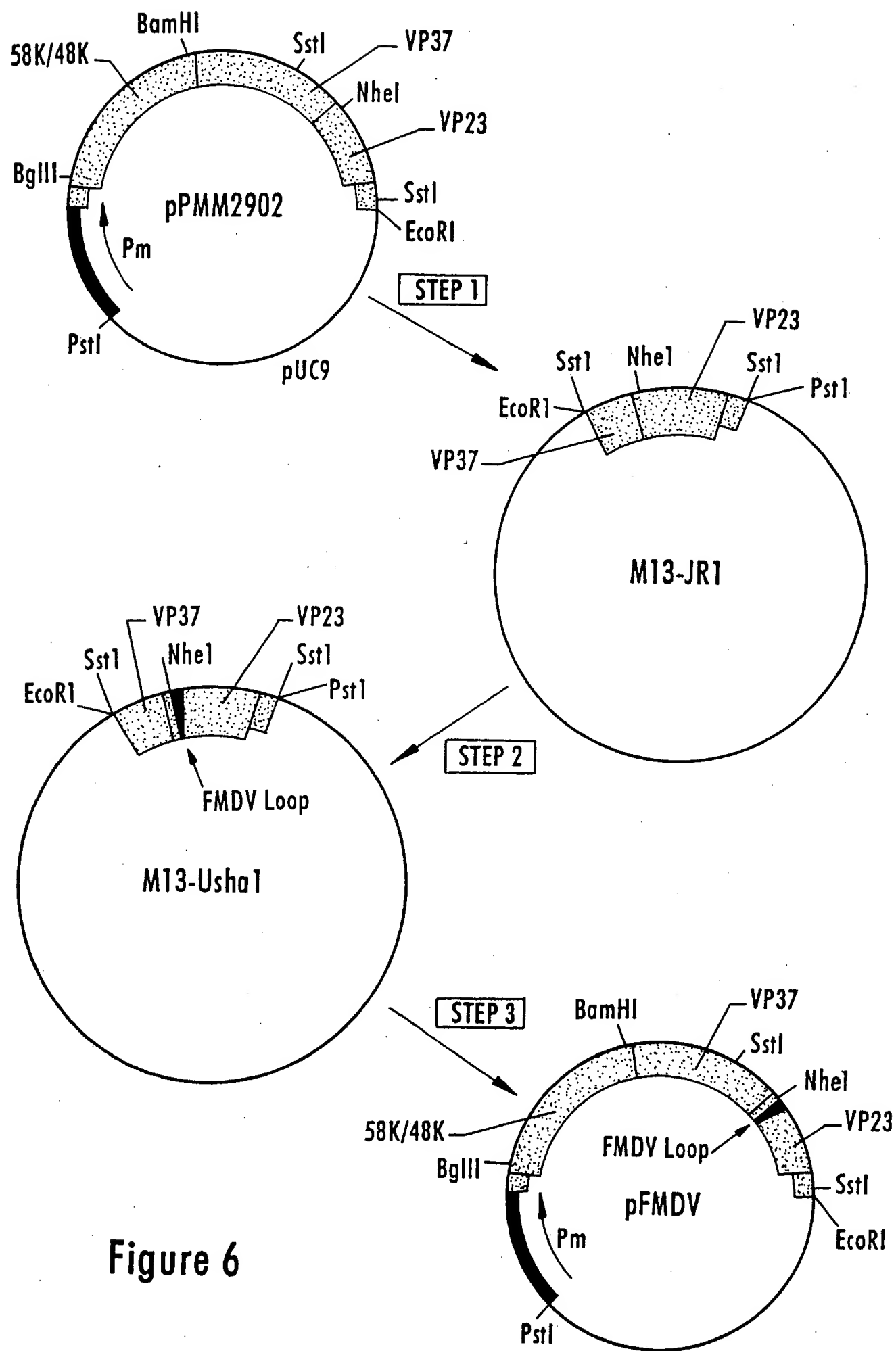
Figure 4

Figure 5(A)

(SEQ ID NO: 7)  
(SEQ ID NO: 8)  
S T Y S R N A V P N L R G D L Q V L A Q K V A R T L P  
CTAGCACTTATAGTAGAAATGCTGTTCCTAATTGAGAGGAGATCTTCAAGTTTGGCTCAAAGGTTGCTCGGACTCTTC  
GTGAATATCATCTTTACGACAAGGATTAAACTCTCCTCTAGAAAGTTCAAACCGAGTTTCCAAACGAGCCTGAGAAAGATC  
BglII (SEQ ID NO: 9)

Figure 5(B)

1 5 10 15 20 25  
G P V C A E A S D V Y S P C M I A S T Y S R N A V P N  
GGACCTGTTTGTGCTGAAGCCTCAGATGTGTATAGCCCATGTATGATAGCTAGCACTTATAGTAGAAATGCTGTCTCCTAAT  
2670 2700 NheI  
-----> 20 25  
L R G D L Q V L A Q K V A R T L P S T P P A P F S (SEQ ID NO: 11)  
TTGAGAGGAGATCTTCAAGTTTGGCTCAAAGGTTGCTCGGACTCTTCCTAGCACTCCTCTGCTCCATTTCCTCA (SEQ ID NO: 10)  
BglII xNheI 2730



**Figure 6**

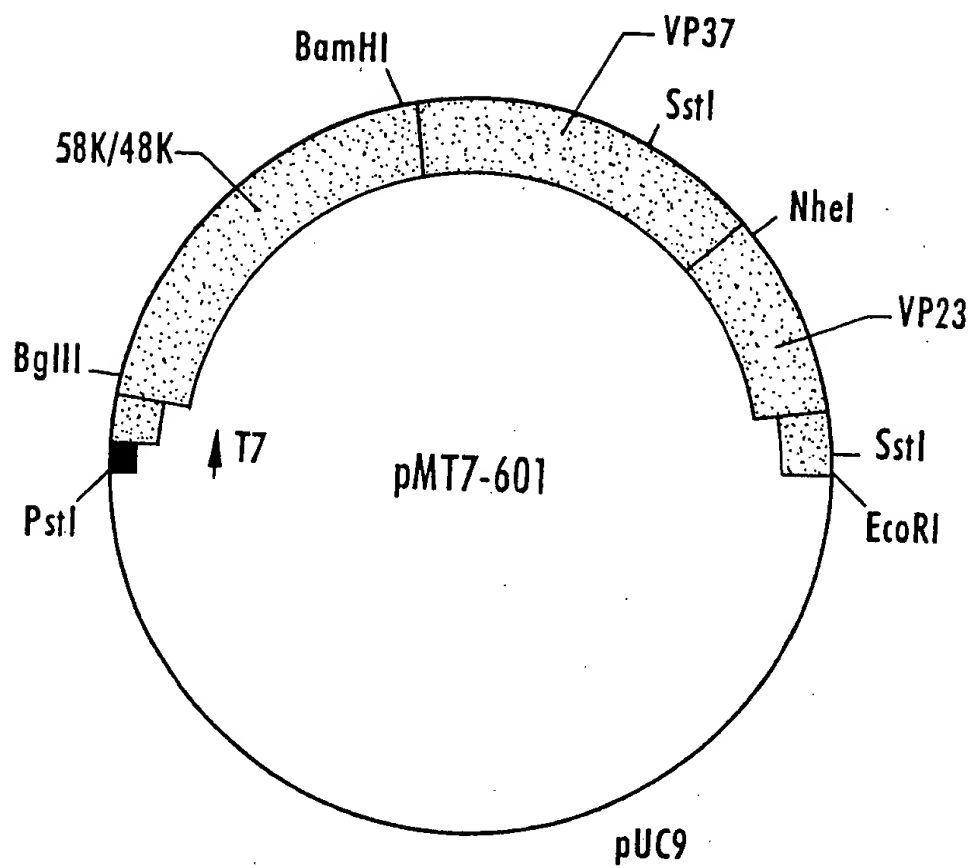


Figure 7

15 P C M I A S T P P A P F S D V T A V T F D L I (SEQ ID NO: 13)  
20 CCATGTATGATAGCTAGCACTCCTCCTGCTCCATTTTCAGACGTTACAGCAGTAACCTTTTGACTTAATC (SEQ ID NO: 12)  
25 2700 NheI 2730 \* 2760

Site-directed  
Mutagenesis



15 P C M I A S T P P A P F S D V T A V T F D L I (SEQ ID NO: 15)  
20 CCATGTATGATAGCTAGCACTCCTCCTGCTCCATTTTCAGACGTCACAGCAGTAACCTTTTGACTTAATC (SEQ ID NO: 14)  
25 2700 NheI 2730 Aat11 2760

Figure 8



Figure 9(A)

S T D R P E G I E E G G E R D R D R S D (SEQ ID NO: 17)  
CTAGCACTGACCGCCCTGAGGGCATCGAGGAAGAGGGCGGTGAGCGGATCGTGATCGTTCCGGACGT (SEQ ID NO: 16)  
GTGACTGGCGGACTCCCGTAGCTCCTTCTCCCGCCACTCGCGCTAGCACTAGCAAGCC (SEQ ID NO: 18)  
PvuI

Figure 9(B)

1 5 10 15 20 25 30 35  
G P V C A E A S D V Y S P C M I A S T D R P E G I E  
GGACCTGTTGTGCTGAAGCCTCAGATGTGTATAGCCCATGTATGATAGCTAGCACTGACCGCCCTGAGGGCATCGAG  
2670 2700 NheI  
-----> 30 35  
E E G G E R D R D R S D V T A V T F D L I (SEQ ID NO: 20)  
GAAGAGGCGGTGAGCGCATCGTGATCGTTCGGACGTCACAGCAGTAACCTTTTGACTTAATC (SEQ ID NO: 19)  
PvuI AatII 2760

Figure 10(A)

S T P A T G I D N H R E A K L D (SEQ ID NO: 22)  
CTAGCACTCCTGCTACTGGAATCGATAATCATAGAGAAGCTAAATTGGACGT (SEQ ID NO: 21)  
GTGAGGACGATGACCTTAGCTATTAGTATCTCTTCGATTAAACC (SEQ ID NO: 23)  
Cla1

Figure 10(B)

1 5 10 15 20 25 30 35  
G P V C A E A S D V Y S P C M I A S T P A T G I D N  
GGACCTGTTTGTGCTGAAGCCTCAGATGTGTATAGCCCATGTATGATAGCTAGCACTCCTGCTACTGGAAATCGATAAT  
2670 2700 Nhe1 Cla1  
-----> 30 35  
H R E A K L D V T A V T F D L I (SEQ ID NO: 25)  
CATAGAGAAGCTAAATTGGACGTACAGCAGTAACTTTGACTTAATC (SEQ ID NO: 24)  
Aat11 2760

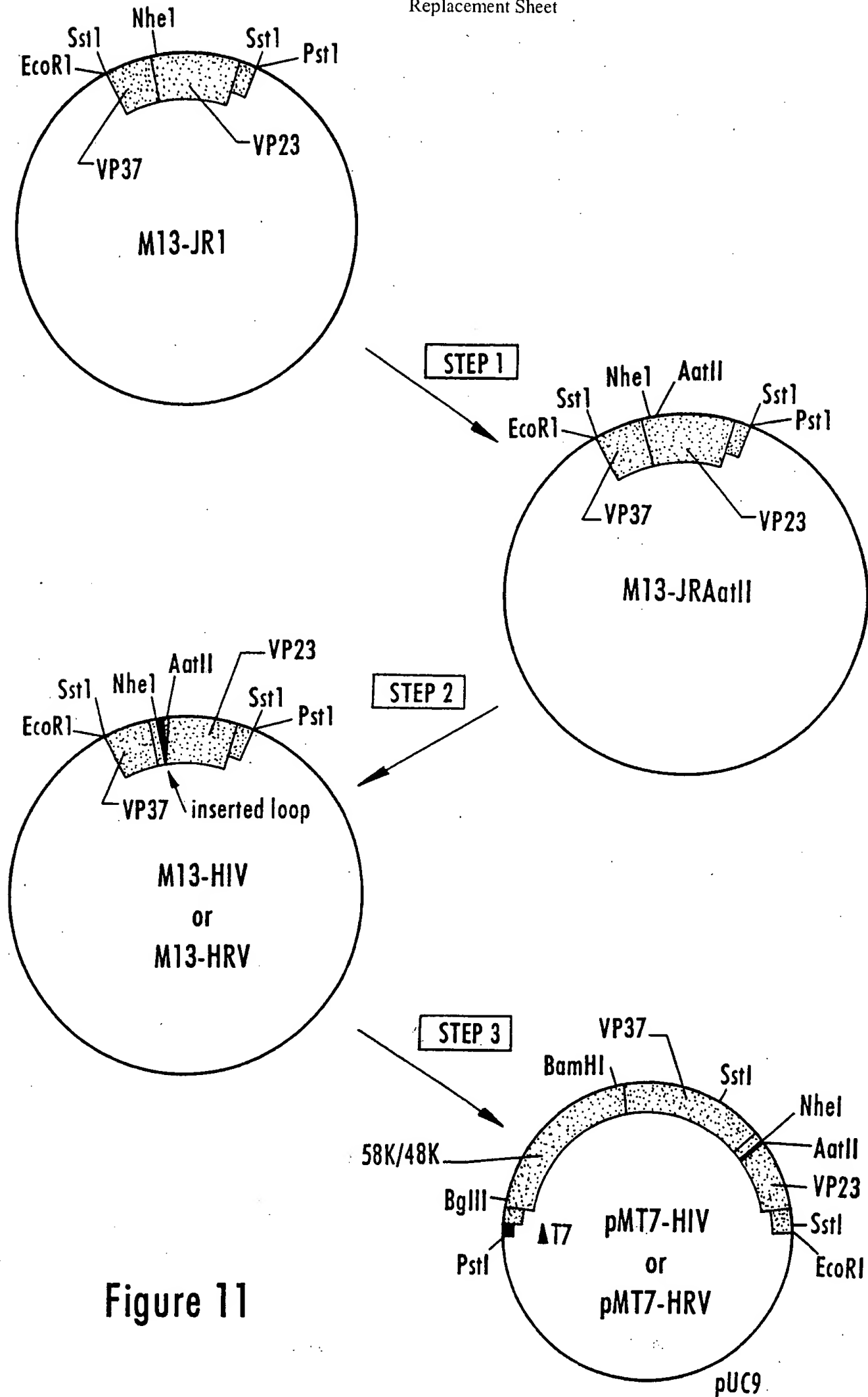


Figure 11

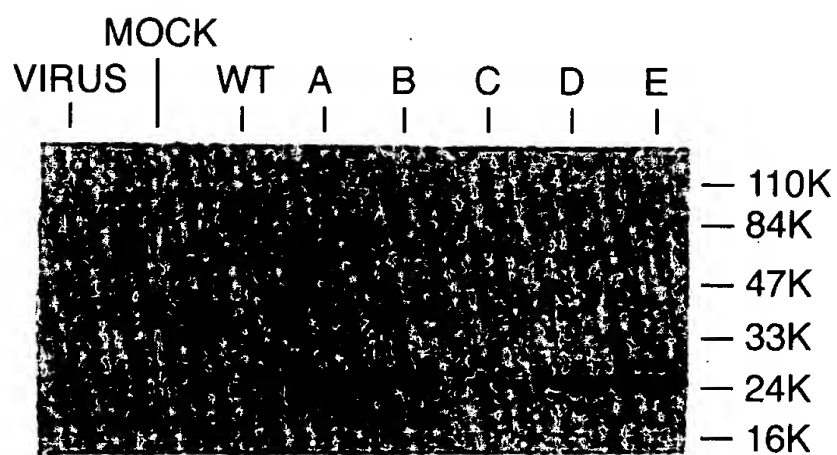


Figure 12